

Table S1: Table presenting percentage homology in nucleotidic (nt, upper part) and in amino acid (aa, lower part) WNV sequences¹.

	WNV-Akela /France/2015, MT863559	WNV-405/04 /France/2004, DQ786572	WNV-PaAn001 /France/2000, AY268132	WNV-7025 /France/2018, MT863561	WNV- Cremona4 /Italy/2014, KP789957
WNV-Akela /France/2015, MT863559		98,55% (10760/10918)	98,31% (10737/10922)	79,72% (8749/10975)	79,79% (8756/10974)
WNV-405/04 /France/2004, DQ786572	99,59 % (3420/3434)		98,54% (10779/10938)	79,65% (8752/10988)	79,72% (8759/10987)
WNV-PaAn001 /France/2000, AY268132	99,74 % (3425/3434)	99,62% (3421/3434)		79,54% (8275/10403)	79,62% (8282/10402)
WNV-7025 /France/2018, MT863561	93,83% (3223/3435)	93,80% (3222/3435)	93,80% (3222/3435)		99,76% (10969/10995)
WNV-Cremona4 /Italy/2014, KP789957	93,97% (3228/3435)	93,94% (3227/3435)	93,94% (3227/3435)	99,76% (3427/3435)	

aa homology

nt homology

¹Whole-genome sequences of recent WNV isolates (WNV-Akela /France/2015 and WNV-7025 /France/2018) were compared to French and Italian complete genome sequences. Pairwise nucleotide and aa sequence alignment were performed with blastn and blastp respectively (<https://blast.ncbi.nlm.nih.gov/>).

Table S2: Amino acid substitutions identified between WNV-Akela/France/2015 and older French lineage 1 isolates

AA position in the WNV polyprotein	Gene	WNV-Akela /France/2015, MT863559	WNV-PaAn001 /France/2000, AY268132	WNV-405/04 /France/2004, DQ786572
100	C	S	S	L
119	C	A	A	T
158	prM	I	I	T
383	E	K	R	R
443	E	G	G	R
602	E	L	L	F
836	NS1	I	V	I
929	NS1	P	P	S
932	NS1	K	K	R
1271	NS2A	E	G	E
1362	NS2A	V	A	A
1749	NS3	H	H	Q
2008	NS3	N	S	N
2288	NS4B	R	S	S
2532	NS5	R	K	K
2572	NS5	K	R	R
2902	NS5	Y	Y	H
3209	NS5	T	I	T
Non synonymous mutations			9	14

Table S3: Amino acid substitutions identified between lineage 2 WNV-7025/France/2018 and the closely genetically related WNV-Cremona4/Italy/2014

AA position in the WNV polyprotein	Gene	WNV-Cremona4 /Italy/2014, KP789957	WNV-7025 /France/2018, MT863561
207	prM	T	P
345	E	D	V
883	NS1	K	E
1340	NS2A	K	X
1726	NS3	V	I
2557	NS5	R	K
2801	NS5	F	L
3322	NS5	V	A
non-synonymous mutations		8	